

SEQUENCE LISTING

<110> The Government of the United States of America, as

<120> MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG AND
SIV ENV GENES

<130> 2026-4287US1 HIV GAG/POL, SIV GAG & ENV

<140> TO BE ASSIGNED

<141> 2001-06-01

<150> PCT/US00/34985

<151> 2000-12-22

<150> 60/173,036

<151> 1999-12-23

<160> 19

<170> PatentIn Ver. 2.1

<210> 1

<211> 4338

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated Human
Immunodeficiency Virus - 1 Gag/Pol gene

<400> 1

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<210> 2

<211> 2507

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 2

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<210> 3

<211> 2467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated Human
Immunodeficiency Virus - 1 Pol gene

<400> 3

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<210> 4

<211> 1533

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated
Simian Immunodeficiency Virus Gag gene

<400> 4

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<210> 5

<211> 1532

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence of mutated Simian Immunodeficiency Virus
Gag gene (SIVgagDX) with wild-type SIV 239 Gag
gene

<400> 5

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acctcaattc tctctttgga ggagaccagt ag 1532

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<210> 6
 <211> 8366
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
 of the construct pCMVgagpolBNKan containing a CMV
 promoter, a HIV gag/pol gene and a kanamycin
 resistance gene

<400> 6

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<210> 10

<211> 122

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
 of the BSSHII to ClaI fragment in transfer
 construct pmBCwCNluci and pmBCmCNluci

<400> 10

cgcgacggc aagaggcgag gggcgggcgcc tgacgaggac gccaaaaatt ttgactagcg 60
 gaggctagaa ggagagagct cgggtgcgaga gcgtcagtat taagcggggg agaattagat 120
 cg 122

<210> 11

<211> 122

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
 of the BSSHII to ClaI fragment in transfer
 construct 3

<400> 11

cgcgacggc aagaggcgag gggcgggcgcc tggggaggac gccaaaaatt ttgactagcg 60
 gaggctagaa ggagagagat ggggtgcgaga gcgtcagtat taagcggggg agaattagat 120
 cg 122

<210> 12

<211> 122

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 12

cgcgacggc aagaggcgag gggcgggcgac tggtagtac gccaaaaatt ttgactatcg 60
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 cg 122

<210> 13
<211> 122
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Plurality
Consensus sequence of DNA sequence of the BSSHII
to CLaI fragment in HIV-1 and transfer constructs

<400> 13
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aa 122

<210> 14
<211> 122
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA sequence
of construct CMVkan/R-R-SIVgp160 CTE

<400> 14
cgcgccacggc aagagggcgag gggcgggcgac tggtagtac gccaaaaatt ttgactagcg 60
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cg 122

<210> 15
<211> 6978
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA sequence
of construct CMVkan/R-R-SIVgp160 CTE

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<210> 16

<211> 879

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SIV gp160env
IN PLASMID CMVkan/R-R-SIVgp160 CTE

<400> 16

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Met Gly Cys Leu Gly Asn Gln Leu Leu Ile Ala Ile Leu Leu Leu Ser
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Val Tyr Gly Ile Tyr Cys Thr Leu Tyr Val Thr Val Phe Tyr Gly Val
      20              25             30

```

```

Pro Ala Trp Arg Asn Ala Thr Ile Pro Leu Phe Cys Ala Thr Lys Asn
      35              40             45

```

```

Arg Asp Thr Trp Gly Thr Thr Gln Cys Leu Pro Asp Asn Gly Asp Tyr
      50              55             60

```

```

Ser Glu Val Ala Leu Asn Val Thr Glu Ser Phe Asp Ala Trp Asn Asn
      65              70             75             80

```

```

Thr Val Thr Glu Gln Ala Ile Glu Asp Val Trp Gln Leu Phe Glu Thr
      85              90             95

```

```

Ser Ile Lys Pro Cys Val Lys Leu Ser Pro Leu Cys Ile Thr Met Arg
      100             105            110

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Cys Asn Lys Ser Glu Thr Asp Arg Trp Gly Leu Thr Lys Ser Ile Thr
115 120 125

Thr Thr Ala Ser Thr Thr Ser Thr Thr Ala Ser Ala Lys Val Asp Met
130 135 140

Val Asn Glu Thr Ser Ser Cys Ile Ala Gln Asp Asn Cys Thr Gly Leu
145 150 155 160

Glu Gln Glu Gln Met Ile Ser Cys Lys Phe Asn Met Thr Gly Leu Lys
165 170 175

Arg Asp Lys Lys Lys Glu Tyr Asn Glu Thr Trp Tyr Ser Ala Asp Leu
180 185 190

Val Cys Glu Gln Gly Asn Asn Thr Gly Asn Glu Ser Arg Cys Tyr Met
195 200 205

Asn His Cys Asn Thr Ser Val Ile Gln Glu Ser Cys Asp Lys His Tyr
210 215 220

Trp Asp Ala Ile Arg Phe Arg Tyr Cys Ala Pro Pro Gly Tyr Ala Leu
225 230 235 240

Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Met Pro Lys Cys Ser
245 250 255

Lys Val Val Val Ser Ser Cys Thr Arg Met Met Glu Thr Gln Thr Ser
260 265 270

Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile
275 280 285

Tyr Trp His Gly Arg Asp Asn Arg Thr Ile Ile Ser Leu Asn Lys Tyr
290 295 300

Tyr Asn Leu Thr Met Lys Cys Arg Arg Pro Gly Asn Lys Thr Val Leu
305 310 315 320

Pro Val Thr Ile Met Ser Gly Leu Val Phe His Ser Gln Pro Ile Asn
325 330 335

Asp Arg Pro Lys Gln Ala Trp Cys Trp Phe Gly Gly Lys Trp Lys Asp
340 345 350

Ala Ile Lys Glu Val Lys Gln Thr Ile Val Lys His Pro Arg Tyr Thr
355 360 365

Gly Thr Asn Asn Thr Asp Lys Ile Asn Leu Thr Ala Pro Gly Gly Gly			
370	375	380	
Asp Pro Glu Val Thr Phe Met Trp Thr Asn Cys Arg Gly Glu Phe Leu			
385	390	395	400
Tyr Cys Lys Met Asn Trp Phe Leu Asn Trp Val Glu Asp Arg Asn Thr			
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Ala Asn Gln Lys Pro Lys Glu Gln His Lys Arg Asn Tyr Val Pro Cys			
	420	425	430
His Ile Arg Gln Ile Ile Asn Thr Trp His Lys Val Gly Lys Asn Val			
	435	440	445
Tyr Leu Pro Pro Arg Glu Gly Asp Leu Thr Cys Asn Ser Thr Val Thr			
450	455	460	
Ser Leu Ile Ala Asn Ile Asp Trp Ile Asp Gly Asn Gln Thr Asn Ile			
465	470	475	480
Thr Met Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp			
	485	490	495
Tyr Lys Leu Val Glu Ile Thr Pro Ile Gly Leu Ala Pro Thr Asp Val			
	500	505	510
Lys Arg Tyr Thr Thr Gly Gly Thr Ser Arg Asn Lys Arg Gly Val Phe			
	515	520	525
Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met Gly			
	530	535	540
Ala Ala Ser Leu Thr Leu Thr Ala Gln Ser Arg Thr Leu Leu Ala Gly			
545	550	555	560
Ile Val Gln Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln			
	565	570	575
Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Thr Arg			
	580	585	590
Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu Asn Ala			
	595	600	605
Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Pro			
610	615	620	

Asn Ala Ser Leu Thr Pro Lys Trp Asn Asn Glu Thr Trp Gln Glu Trp
 625 630 635 640

Glu Arg Lys Val Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu Leu Glu
 645 650 655

Glu Ala Gln Ile Gln Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu
 660 665 670

Asn Ser Trp Asp Val Phe Gly Asn Trp Phe Asp Leu Ala Ser Trp Ile
 675 680 685

Lys Tyr Ile Gln Tyr Gly Val Tyr Ile Val Val Gly Val Ile Leu Leu
 690 695 700

Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ala Lys Leu Arg Gln Gly
 705 710 715 720

Tyr Arg Pro Val Phe Ser Ser Pro Pro Ser Tyr Phe Gln Gln Thr His
 725 730 735

Ile Gln Gln Asp Pro Ala Leu Pro Thr Arg Glu Gly Lys Glu Arg Asp
 740 745 750

Gly Gly Glu Gly Gly Gly Asn Ser Ser Trp Pro Trp Gln Ile Glu Tyr
 755 760 765

Ile His Phe Leu Ile Arg Gln Leu Ile Arg Leu Leu Thr Trp Leu Phe
 770 775 780

Ser Asn Cys Arg Thr Leu Leu Ser Arg Val Tyr Gln Ile Leu Gln Pro
 785 790 795 800

Ile Leu Gln Arg Leu Ser Ala Thr Leu Gln Arg Ile Arg Glu Val Leu
 805 810 815

Arg Thr Glu Leu Thr Tyr Leu Gln Tyr Gly Trp Ser Tyr Phe His Glu
 820 825 830

Ala Val Gln Ala Val Trp Arg Ser Ala Thr Glu Thr Leu Ala Gly Ala
 835 840 845

Trp Gly Asp Leu Trp Glu Thr Leu Arg Arg Gly Gly Arg Trp Ile Leu
 850 855 860

Ala Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Leu Thr Leu Leu
 865 870 875

210	215	220
Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser		
225	230	235 240
Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro		
245	250	255
Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe		
260	265	270

<210> 18
 <211> 2640
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: DNA sequence
 of mutated SIV gene in construct
 CMVkan/R-R-SIVgp160 CTE

<400> 18

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